

CLAIMS

1. A polypeptide having cellobiohydrolase II activity, selected from the group consisting of:

- 5 (a) a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 75%, identity with the amino acid sequence shown as amino acids 1 to 477 of SEQ ID NO:2,
a polypeptide comprising an amino acid sequence selected from the group consisting of:
10 an amino acid sequence which has at least 85% identity with the partial amino acid sequence shown as amino acids 1 to 82 of SEQ ID NO:4,
a polypeptide comprising an amino acid sequence selected from the group consisting of:
15 an amino acid sequence which has at least 85% identity with the amino acid sequence shown as amino acids 1 to 420 of SEQ ID NO:4,
a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 80% identity with the partial amino acid sequence shown as amino acids 1 to 139 of SEQ ID NO:6,
20 a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 95% identity with the partial amino acid sequence shown as amino acids 1 to 102 of SEQ ID NO:8,
25 a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 85% identity with the partial amino acid sequence shown as amino acids 1 to 144 of SEQ ID NO:10,
a polypeptide comprising an amino acid sequence selected from the group consisting of:
30 an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 99 of SEQ ID NO:12,
a polypeptide comprising an amino acid sequence selected from the group consisting of:
35 an amino acid sequence which has at least 85% identity with the partial amino acid sequence shown as amino acids 1 to 140 of SEQ ID NO:14,
a polypeptide comprising an amino acid sequence selected from the group consisting

of:

an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 109 of SEQ ID NO:16,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 407 of SEQ ID NO:16,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 143 of SEQ ID NO:18,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 70% identity with the partial amino acid sequence shown as amino acids 1 to 71 of SEQ ID NO:20,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 60% identity with the amino acid sequence shown as amino acids 1 to 220 of SEQ ID NO:22,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 65% identity with the amino acid sequence shown as amino acids 1 to 458 of SEQ ID NO:24, and

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 70% identity with the amino acid sequence shown as amino acids 1 to 390 of SEQ ID NO:26,

(b) a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Chaetomium thermophilum*,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 85% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in

Myceliophthora thermophila,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Melanocarpus albomyces*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Acremonium thermophilum*,

an amino acid sequence which has at least 95% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Melanocarpus* sp.,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Thielavia microspora*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Aspergillus fumigatus*,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Aspergillus* sp.,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Thielavia australiensis*,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Aspergillus tubingensis*,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Gloeophyllum trabeum*,

an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Meripilus giganteus*,

an amino acid sequence which has at least 60% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Trichophaea saccata*,

an amino acid sequence which has at least 65% identity with the polypeptide encoded

by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Stilbella annulata*, and

an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Malbranchea cinnamomea*.

(c) a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 63 to 1493 of SEQ ID NO:1,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 85% identity with the polypeptide encoded by nucleotides 1 to 246 of SEQ ID NO:3,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 80% identity with the polypeptide encoded by nucleotides 1 to 417 of SEQ ID NO:5,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 95% identity with the polypeptide encoded by nucleotides 1 to 306 of SEQ ID NO:7,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 85% identity with the polypeptide encoded by nucleotides 1 to 432 of SEQ ID NO:9,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 1 to 297 of SEQ ID NO:11,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 85% identity with the polypeptide encoded by nucleotides 1 to 420 of SEQ ID NO:13,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the polypeptide encoded

by nucleotides 1 to 330 of SEQ ID NO:15,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 1 to 1221 of SEQ ID NO:15,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 1 to 429 of SEQ ID NO:17,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 70% identity with the polypeptide encoded by nucleotides 1 to 213 of SEQ ID NO:19,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 60% identity with the polypeptide encoded by nucleotides 43 to 701 of SEQ ID NO:21,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 65% identity with the polypeptide encoded by nucleotides 21 to 1394 of SEQ ID NO:23, and

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 70% identity with the polypeptide encoded by nucleotides 41 to 1210 of SEQ ID NO:25,

(d) a polypeptide which is encoded by a nucleotide sequence which hybridizes under high stringency conditions with a polynucleotide probe selected from the group consisting of:

(i) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 1493 of SEQ ID NO:1,

nucleotides 1 to 246 of SEQ ID NO:3,

nucleotides 1 to 1272 of SEQ ID NO:3,

nucleotides 1 to 417 of SEQ ID NO:5,

nucleotides 1 to 306 of SEQ ID NO:7,

nucleotides 1 to 432 of SEQ ID NO:9,

nucleotides 1 to 297 of SEQ ID NO:11,

- nucleotides 1 to 420 of SEQ ID NO:13,
nucleotides 1 to 330 of SEQ ID NO:15,
nucleotides 1 to 1221 of SEQ ID NO:15,
nucleotides 1 to 429 of SEQ ID NO:17,
5 nucleotides 1 to 213 of SEQ ID NO:19,
nucleotides 43 to 701 of SEQ ID NO:21,
nucleotides 21 to 1394 of SEQ ID NO:23, and
nucleotides 41 to 1210 of SEQ ID NO:25.
- 10 (ii) the complementary strand of the nucleotides selected from the group consisting of:
nucleotides 63 to 563 of SEQ ID NO:1,
nucleotides 43 to 543 of SEQ ID NO:21,
nucleotides 21 to 521 of SEQ ID NO:23, and
nucleotides 41 to 541 of SEQ ID NO:25.
- 15 (iii) the complementary strand of the nucleotides selected from the group consisting of:
nucleotides 63 to 263 of SEQ ID NO:1,
nucleotides 1 to 200 of SEQ ID NO:3,
nucleotides 1 to 1272 of SEQ ID NO:3,
20 nucleotides 1 to 200 of SEQ ID NO:5,
nucleotides 1 to 200 of SEQ ID NO:5,
nucleotides 1 to 200 of SEQ ID NO:7,
nucleotides 1 to 200 of SEQ ID NO:9,
nucleotides 1 to 200 of SEQ ID NO:13,
25 nucleotides 1 to 200 of SEQ ID NO:11,
nucleotides 1 to 200 of SEQ ID NO:13,
nucleotides 1 to 200 of SEQ ID NO:15,
nucleotides 1 to 1221 of SEQ ID NO:15
nucleotides 1 to 200 of SEQ ID NO:17,
30 nucleotides 1 to 200 of SEQ ID NO:19,
nucleotides 43 to 243 of SEQ ID NO:21,
nucleotides 21 to 221 of SEQ ID NO:23, and
nucleotides 41 to 241 of SEQ ID NO:25.
- 35 (e) a fragment of (a), (b) or (c) that has cellobiohydrolase II activity.

2. The polypeptide according to claim 1, comprising an amino acid sequence selected from

the group consisting of:

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 80% identity, preferably 85% identity, more preferably 85% identity, even more preferably at least 90% identity, most preferably at least 95% identity with the amino acid sequence shown as amino acids 1 to 477 of SEQ ID NO:2,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 90% identity, preferably 95% identity with the partial amino acid sequence shown as amino acids 1 to 82 of SEQ ID NO:4,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 90% identity, preferably 95% identity with the amino acid sequence shown as amino acids 1 to 420 of SEQ ID NO:4,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 85% identity, preferably 90% identity, more preferably 95% identity with the partial amino acid sequence shown as amino acids 1 to 156 of SEQ ID NO:6,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 80% identity, preferably 85% identity, more preferably 85% identity, even more preferably at least 90% identity, identity with the partial amino acid sequence shown as amino acids 1 to 139 of SEQ ID NO:6,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 96% identity, preferably 97% identity, more preferably 98% identity, and most preferably 99% identity with the partial amino acid sequence shown as amino acids 1 to 102 of SEQ ID NO:8,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at 90% identity, preferably 95% identity with the partial amino acid sequence shown as amino acids 1 to 144 of SEQ ID NO:10,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 80% identity, preferably 85% identity, more

preferably 85% identity, even more preferably at least 90% identity, most preferably 95% identity with the partial amino acid sequence shown as amino acids 1 to 99 of SEQ ID NO:12,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 90% identity, preferably 95% identity with the partial amino acid sequence shown as amino acids 1 to 140 of SEQ ID NO:14,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 80% identity, preferably 85% identity, more preferably 85% identity, even more preferably at least 90% identity, most preferably 95% identity with the partial amino acid sequence shown as amino acids 1 to 109 of SEQ ID NO:16,

an amino acid sequence which has at least 80% identity, preferably 85% identity, more preferably 85% identity, even more preferably at least 90% identity, most preferably 95% identity with the amino acid sequence shown as amino acids 1 to 407 of SEQ ID NO:16,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 80% identity, preferably 85% identity, more preferably 85% identity, even more preferably at least 90% identity with the partial amino acid sequence shown as amino acids 1 to 143 of SEQ ID NO:18,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity, preferably 80% identity, more preferably 85% identity, even more preferably 85% identity, most preferably at least 90% identity, and yet more preferably at least 95% identity with the partial amino acid sequence shown as amino acids 1 to 71 of SEQ ID NO:20,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 60% identity, preferably 65% identity, more preferably 70% identity, even more preferably 75% identity, most preferably 80% identity, yet more preferably 85% identity, such as even at least 85% identity, or least 90% identity, or at least 95% identity with the partial amino acid sequence shown as amino acids 1 to 220 of SEQ ID NO:22,

a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 65% identity, preferably 70% identity, more preferably 75% identity, even more preferably 80% identity, yet more preferably 85% identity, such as even at least 85% identity, or least 90% identity, or at least 95% with the amino acid sequence shown as amino acids 1 to 458 of SEQ ID NO:24, and

5 a polypeptide comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 75% identity, preferably 80% identity, more preferably 85% identity, even more preferably 85% identity, most preferably at least 90% identity, and yet more preferably at least 95% identity with the amino acid
10 sequence shown as amino acids 1 to 390 of SEQ ID NO:26.

3. The polypeptide according to any of claims 1-2, where the polypeptide is an artificial variant which comprises an amino acid sequence that has at least one substitution, deletion and/or insertion of an amino acid as compared to an amino acid sequence
15 selected from the group consisting of:

amino acids 1 to 477 of SEQ ID NO:2,
amino acids 1 to 82 of SEQ ID NO:4,
amino acids 1 to 420 of SEQ ID NO:4,
amino acids 1 to 139 of SEQ ID NO:6,
20 amino acids 1 to 102 of SEQ ID NO:8,
amino acids 1 to 144 of SEQ ID NO:10,
amino acids 1 to 99 of SEQ ID NO:12,
amino acids 1 to 140 of SEQ ID NO:14,
amino acids 1 to 109 of SEQ ID NO:16,
25 amino acids 1 to 407 of SEQ ID NO:16,
amino acids 1 to 143 of SEQ ID NO:18,
amino acids 1 to 71 of SEQ ID NO:20,
amino acids 1 to 220 of SEQ ID NO:22,
amino acids 1 to 458 of SEQ ID NO:24, and
30 amino acids 1 to 390 of SEQ ID NO:26.

4. A polynucleotide having a nucleotide sequence which encodes for the polypeptide defined in any of claims 1-3.

35 5. A nucleic acid construct comprising the nucleotide sequence defined in claim 4 operably linked to one or more control sequences that direct the production of the polypeptide in a suitable host.

6. A recombinant expression vector comprising the nucleic acid construct defined in claim 5.

7. A recombinant host cell comprising the nucleic acid construct defined in claim 5.

5

8. A method for producing a polypeptide as defined in any of claims 1-3, the method comprising:

(a) cultivating a strain, which in its wild-type form is capable of producing the polypeptide, to produce the polypeptide; and

10 (b) recovering the polypeptide.

9. A method for producing a polypeptide as defined in any of claims 1-3, the method comprising:

15 (a) cultivating a recombinant host cell as defined in claim 7 under conditions conducive for production of the polypeptide; and

(b) recovering the polypeptide.

10. A method for in-situ production of a polypeptide as defined in any of claims 1-3, the method comprising:

20 (a) cultivating a recombinant host cell as defined in claim 7 under conditions conducive for production of the polypeptide; and

(b) contacting the polypeptide with a desired substrate without prior recovery of the polypeptide.

25 11. A polynucleotide comprising a nucleotide sequence which has at least 80%, preferably at least 85%, more preferably 90% identity, most preferably 95% identity with a nucleotide selected from the group consisting of:

nucleotides 63 to 1493 of SEQ ID NO:1,

nucleotides 1 to 246 of SEQ ID NO:3,

30 nucleotides 1 to 1272 of SEQ ID NO:3,

nucleotides 1 to 417 of SEQ ID NO:5,

nucleotides 1 to 306 of SEQ ID NO:7,

nucleotides 1 to 432 of SEQ ID NO:9,

nucleotides 1 to 297 of SEQ ID NO:11,

35 nucleotides 1 to 420 of SEQ ID NO:13,

nucleotides 1 to 330 of SEQ ID NO:15,

nucleotides 1 to 1221 of SEQ ID NO:15

nucleotides 1 to 429 of SEQ ID NO:17,
nucleotides 1 to 213 of SEQ ID NO:19,
nucleotides 43 to 701 of SEQ ID NO:21,
nucleotides 21 to 1394 of SEQ ID NO:23, and
nucleotides 41 to 1210 of SEQ ID NO:25.

12. A polynucleotide having a nucleotide sequence which encodes a polypeptide having cellobiohydrolase II activity, and which hybridizes under high stringency conditions with a polynucleotide probe selected from the group consisting of:

(i) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 1493 of SEQ ID NO:1,
nucleotides 1 to 246 of SEQ ID NO:3,
nucleotides 1 to 1272 of SEQ ID NO:3,
nucleotides 1 to 417 of SEQ ID NO:5,
nucleotides 1 to 306 of SEQ ID NO:7,
nucleotides 1 to 432 of SEQ ID NO:9,
nucleotides 1 to 297 of SEQ ID NO:11,
nucleotides 1 to 420 of SEQ ID NO:13,
nucleotides 1 to 330 of SEQ ID NO:15,
nucleotides 1 to 1221 of SEQ ID NO:15,
nucleotides 1 to 429 of SEQ ID NO:17,
nucleotides 1 to 213 of SEQ ID NO:19,
nucleotides 43 to 701 of SEQ ID NO:21,
nucleotides 21 to 1394 of SEQ ID NO:23, and
nucleotides 41 to 1210 of SEQ ID NO:25.

(ii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 563 of SEQ ID NO:1,
nucleotides 43 to 543 of SEQ ID NO:21,
nucleotides 21 to 521 of SEQ ID NO:23, and
nucleotides 41 to 541 of SEQ ID NO:25.

(iii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 263 of SEQ ID NO:1,
nucleotides 1 to 200 of SEQ ID NO:3,
nucleotides 1 to 200 of SEQ ID NO:5,
nucleotides 1 to 200 of SEQ ID NO:7,

nucleotides 1 to 200 of SEQ ID NO:9,
 nucleotides 1 to 200 of SEQ ID NO:11,
 nucleotides 1 to 200 of SEQ ID NO:13,
 nucleotides 1 to 200 of SEQ ID NO:15,
 5 nucleotides 1 to 1221 of SEQ ID NO:15
 nucleotides 1 to 200 of SEQ ID NO:17,
 nucleotides 1 to 200 of SEQ ID NO:19,
 nucleotides 43 to 243 of SEQ ID NO:21,
 nucleotides 21 to 221 of SEQ ID NO:23, and
 10 nucleotides 41 to 241 of SEQ ID NO:25.

13. A polynucleotide comprising a modified nucleotide sequence selected from the group consisting of:

the nucleotide sequence of SEQ ID NO:1 comprising at least one modification, where
 15 the modified nucleotide sequence encodes a polypeptide comprising the amino acid
 sequence shown in SEQ ID NO:2,
 the nucleotide sequence of SEQ ID NO:3 comprising at least one modification, where
 the modified nucleotide sequence encodes a polypeptide comprising the partial amino
 acid sequence shown in amino acids 1 to 82 of SEQ ID NO:4,
 20 the nucleotide sequence of SEQ ID NO:3 comprising at least one modification, where
 the modified nucleotide sequence encodes a polypeptide comprising the amino acid
 sequence shown in SEQ ID NO:4,
 the nucleotide sequence of SEQ ID NO:5 comprising at least one modification, where
 the modified nucleotide sequence encodes a polypeptide comprising the partial amino
 25 acid sequence shown in SEQ ID NO:6,
 the nucleotide sequence of SEQ ID NO:7 comprising at least one modification, where
 the modified nucleotide sequence encodes a polypeptide comprising the partial amino
 acid sequence shown in SEQ ID NO:8,
 the nucleotide sequence of SEQ ID NO:9 comprising at least one modification, where
 30 the modified nucleotide sequence encodes a polypeptide comprising the partial amino
 acid sequence shown in SEQ ID NO:10,
 the nucleotide sequence of SEQ ID NO:13 comprising at least one modification, where
 the modified nucleotide sequence encodes a polypeptide comprising the partial amino
 acid sequence shown in SEQ ID NO:14,
 35 the nucleotide sequence of SEQ ID NO:11 comprising at least one modification, where
 the modified nucleotide sequence encodes a polypeptide comprising the partial amino
 acid sequence shown in SEQ ID NO:12,

the nucleotide sequence of SEQ ID NO:13 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide comprising the partial amino acid sequence shown in SEQ ID NO:14,

the nucleotide sequence 1 to 330 of SEQ ID NO:15 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide comprising the partial amino acid sequence shown in 1 to 109 of SEQ ID NO:16,

the nucleotide sequence of SEQ ID NO:15 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NO:16,

the nucleotide sequence of SEQ ID NO:17 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 450 of SEQ ID NO:18,

the nucleotide sequence of SEQ ID NO:19 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide comprising the partial amino acid sequence shown in SEQ ID NO:20,

the nucleotide sequence of SEQ ID NO:21 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide comprising the partial amino acid sequence shown in SEQ ID NO:22,

the nucleotide sequence of SEQ ID NO:23 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NO:24, and

the nucleotide sequence of SEQ ID NO:25 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NO:26.

14. A polypeptide having cellobiohydrolase II activity which is encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in a microorganism selected from the group consisting of:

a microorganism belonging to the family *Chaetomiaceae*, preferably to the genus *Chaetomium*, more preferably to the species *Chaetomium thermophilum*,

a microorganism belonging to the genus *Myceliophthora*, preferably to the species *Myceliophthora thermophila*,

a microorganism belonging to the species *Acremonium thermophilum*,

a microorganism belonging to the family *Chaetomiaceae*, preferably to the genus *Thielavia*, preferably to the species *Thielavia australiensis*

a microorganism belonging to the genus *Aspergillus*, preferably belonging to the black *Aspergilli* (subgenus *circumdati*, section *nigr*)

a microorganism belonging to the family Chaetomiaceae, preferably to the genus *Thielavia*, preferably to the species *Thielavia microspore*,

5 a microorganism belonging to the genus *Aspergillus*, preferably belonging to the black *Aspergilli*, more preferably to the species *Aspergillus tubingensis*, and most preferably to the species *A. neotubingensis* Frisvad sp.nov.

10 a microorganism belonging to the *Polyporales*, preferably belonging to the family *Fomitopsidaceae*, more preferably belonging to the genus *Gloeophyllum*, most preferably to the species *Gloeophyllum trabeum*

a microorganism belonging to the *Hymenochaetales*, preferably belonging to the family *Rigidiporaceae*, preferably belonging to the genus *Meripilus*, more preferably to the species *Meripilus giganteus*,

15 a microorganism belonging to the *Pezizomycotina*, preferably belonging to *Pezizales*, preferably belonging to the family *Pyronemataceae* or the family *Sarcosomataceae*, more preferably belonging to the genus *Trichophaea* or the genus *Pseudoplectania*, most preferably *Trichophaea saccata*,

a microorganism belonging to the species *Stilbella annulata*, and

a microorganism belonging to the species *Malbrancheae cinnamomea*.

20

15. A method for shuffling of DNA comprising using the polynucleotide as defined in any of claims 4 and 11-13.

25 16. A polynucleotide encoding a polypeptide having cellobiase activity obtainable by the method of claim 15.

17. A polypeptide having cellobiase activity encoded by the polynucleotide of claim 16.

18. Use of the polynucleotide as defined in any of claims 4 and 11-13 for DNA shuffling.

30

19. A method for producing ethanol from biomass, comprising contacting the biomass with the polypeptide as defined in any of claims 1-3.

20. Use of the polypeptide as defined in any of claims 1-3 for producing ethanol.

21. A transgenic plant, plant part or plant cell, which has been transformed with a nucleotide sequence encoding a polypeptide having cellobiohydrolase II activity as defined in any of
5 claims 1- 3.

22. A detergent composition comprising a surfactant and the polypeptide according to any of claims 1-3.